

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 17, 2003, 16:09:08 ; Search time 11 Seconds
(without alignments)
912.479 Million cell updates/sec

Title: US-09-978-309a-74

Sequence: 1 OEKIDSMVSLSDVTAQFES.....KKKQSETKLOELNKVLGIK 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1193	99.8	724	1	HMNR_HUMAN
2	913	76.4	794	1	HMNR_MOUSE
3	897	75.1	498	1	HMNR_RAT
4	191	16.0	976	1	SCPI_HUMAN
5	185.5	15.5	1790	1	USOI_YEAST
6	182.5	15.3	1938	1	MYH4_YEAST
7	181.5	15.2	1940	1	MYH4_RABIT
8	180.5	15.1	1941	1	MYH2_HUMAN
9	179.5	15.0	1938	1	MYSS_CHICK
10	179.5	15.0	1939	1	MYH4_HUMAN
11	179	15.0	697	1	MEPI_LYCES
12	178.5	14.9	1939	1	MYH1_HUMAN
13	178.5	14.9	1940	1	MYH3_HUMAN
14	176.5	14.8	845	1	SCPI_MESAU
15	176.5	14.8	1937	1	MYH8_HUMAN
16	176.5	14.8	1940	1	MYH3_CHICK
17	175	14.6	993	1	SCPI_MOUSE
18	172.5	14.4	864	1	RA50_SULISO
19	172.5	14.4	865	1	MYSP_SCHMA
20	171.5	14.4	1935	1	MYSS_CYPCA
21	171	14.3	886	1	MYSS_CYPCA
22	169	14.1	2230	1	GOG4_HUMAN
23	167	14.0	2245	1	MYSD_DICDI
24	166.5	13.9	1102	1	MYSS_RABIT
25	166.5	13.9	1102	1	MYSS_CHICK
26	165.5	13.8	879	1	MYSC_SULTO
27	162.5	13.6	1938	1	MYH6_MOUSE
28	162.5	13.6	1939	1	MYH6_HUMAN
29	162	13.6	1935	1	MYH7_PIG
30	161.5	13.5	1938	1	MYH6_RAT
31	161.5	13.5	1939	1	MYH6_MESAU
32	161	13.5	866	1	MYSP_SCHMA
33	161	13.5	1935	1	MYH7_HUMAN

34	160.5	13.4	1286	1	CTRO_HUMAN	O14578	homo sapien
35	160	13.4	1679	1	YIO9_YEAST	P40457	saccharomyc
36	160	13.4	1935	1	MYH7_RAT	P02564	rattus norv
37	160	13.4	1978	1	MYH8_CHICK	P10587	rattus norv
38	159.5	13.3	1597	1	CTRO_MOUSE	P10587	rattus norv
39	159.5	13.3	1938	1	MYH8_HUMAN	P49025	mus musculu
40	158	13.2	978	1	RA50_AOUAE	O67124	aquilex aeo
41	158	13.2	1203	1	SCPE_XENLA	P50533	xenopus lae
42	157.5	13.2	997	1	SCPI_RAT	003410	rattus norv
43	156.5	13.1	886	1	RA50_ARCFU	029230	archaeoglob
44	156.5	13.1	1325	1	G160_MOUSE	P55937	mus musculu
45	155.5	13.0	1957	1	YD86_SCHPO	Q10411	schizosacch

ALIGNMENTS

RESULT 1	HMNR_HUMAN	STANDARD:	PRT:	724 AA.
ID	HMNR_HUMAN	AC_075330: 092767;		
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Hyaluronan mediated motility receptor (intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility) (CD168 antigen).			
DE	antigen).			
CN	HMNR OR IHABP OR RHAMM.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION.			
RC	TISSUE=breast carcinoma;			
RA	Medline=98264864; PubMed=9601098;			
RA	Assmann V., Marshall J.F., Fieber C., Hofmann M., Hart I.R.;			
RT	"The human hyaluronan receptor RHAMM is expressed as an intracellular protein in breast cancer cells."			
RL	J. Cell Sci. 111:1685-1694(1998).			
RP	[2]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=breast;			
RA	Medline=97045829; PubMed=8890751;			
RA	Wang C., Entwistle J., Hou G., Li O., Turley E.A.;			
RT	"The characterization of a human RHAMM cDNA: conservation of the hyaluronan-binding domains."			
RL	Gene 174:299-306(1996).			
CC	- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO HMNR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY.			
CC	- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.			
CC	- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC (BY SIMILARITY).			
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	- TISSUE SPECIFICITY: EXPRESSED IN BREAST CANCER CELL LINES AND IN NORMAL BREAST TISSUE.			
CC	- DATABASE: NAME=PROW; NOTE=PROW 2:76-84(2001); WWW="http://www.ncbi.nlm.nih.gov/prov/guide/80286666.g.htm".			
CC	-----			
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CC	EMBL: AF032862; AAC32548.1;			
CC	EMBL: U29343; AAC52049.1;			

DR Genew; HGNC:5012; HMMR.
 DR MIM; 600936; -
 KW Hyaluronic acid; Alternative splicing; Repeat: Glycoprotein; Antigen.
 FT DOMAIN 635 645 HYALURONIC ACID-BINDING (POTENTIAL).
 FT CARBOHYD 657 666 HYALURONIC ACID-BINDING (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 588 588 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 75 90 MISSING (IN ISOFORM B).
 FT CONFLICT 75 75 K -> KR (IN REF. 2).
 FT CONFLICT 103 103 S -> R (IN REF. 2).
 FT CONFLICT 277 277 E -> D (IN REF. 2).
 FT CONFLICT 298 298 K -> T (IN REF. 2).
 FT CONFLICT 322 322 K -> E (IN REF. 2).
 FT CONFLICT 330 332 OER -> REH (IN REF. 2).
 SQ SEQUENCE 724 AA; 84031 MW; EA68AD6D2A626926 CRC64;

Query Match 99.8%; Score 1193; DB 1; Length 724;
 Best Local Similarity 99.6%; Pred. No. 6.5e-54;
 Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QERYDSWVQSLVDVTAQFESYKALTSIEDLKLENSLOEKAKAKNAEDVQHLLAT 60
 DB 442 QERYDSWVQSLVDVTAQFESYKALTSIEDLKLENSLOEKAKAKNAEDVQHLLAT 501
 QY 61 ESSNOEYVRMLDLQTKSAKTEIKETITVSFLQKTTDLONOLKOEEDFRKOLEDEGR 120
 DB 502 ESSNOEYVRMLDLQTKSAKTEIKETITVSFLQKTTDLONOLKOEEDFRKOLEDEGR 561
 QY 121 KAEKENTTAELTEINKKRLTYEELYNKTRPQIOLDAFEVEKQALLNEGAQEOENKI 180
 DB 562 KAEKENTTAELTEINKKRLTYEELYNKTRPQIOLDAFEVEKQALLNEGAQEOENKI 621
 QY 181 RDSYAKLLGHQNLKQIKIHVYKTKLKDENSQKSEVSKIRCOLAKKQSEKLOEELNKVIG 240
 DB 622 RDSYAKLLGHQNLKQIKIHVYKTKLKDENSQKSEVSKIRCOLAKKQSEKLOEELNKVIG 681
 QY 241 IK 242
 DB 682 IK 683

RESULT 2
 HMMR MOUSE STANDARD; PRT; 794 AA.
 ID HMMR MOUSE
 AC 000547;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hyaluronan mediated motility receptor (intracellular hyaluronate acid binding protein) (Receptor for hyaluronan-mediated motility).
 GN HMMR OR IHABP OR RHAMM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
 RC TISSUE=Lung;
 RA MEDLINE=98264863; PubMed=9601097;
 RA Hofmann M., Fieber C., Assmann V., Goettlicher M., Sleeman J.,
 RA Plug R., Howells N., von Stein O., Ponta H., Herrlich P.;
 RT "Identification of IHABP, a 95 kDa intracellular hyaluronate binding protein";
 RL J. Cell Sci. 111:1673-1684(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhao Y., Zhang S., Turley E.;
 RL Submitted (Jul-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-183 FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN=129/Sv;

RX MEDLINE=99107769; PubMed=98893113;
 RA Fieber C., Plug R., Sleeman J., Dall P., Ponta H., Hofmann M.;
 RT "Characterization of the murine gene encoding the intracellular
 RT hyaluronan receptor IHABP";
 RL Gene 226:41-50(1999).
 RN [4]
 RP SEQUENCE OF 164-794 FROM N.A., AND ALTERNATIVE SPLICING;
 RC STRAIN=BALB/c; TISSUE=Fibroblast;
 RX MEDLINE=96011639; PubMed=7590272;
 RA Entwistle J., Zhang S., Yang B., Wong C., Li Q., Hall C.L., A.J.;
 RA Mowat M., Greenberg A.H., Turley E.A.;
 RT "Characterization of the murine gene encoding the hyaluronan receptor
 RT RHAMM";
 RL Gene 163:233-238(1995).
 RN [5]
 RP SEQUENCE OF 318-794 FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=BALB/c;
 RX MEDLINE=92293690; PubMed=1376732;
 RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,
 RA Clippes V., Austen L., Nance D.M., Turley E.A.;
 RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor
 RT cell motility";
 RL J. Cell Biol. 117:1343-1350(1992).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=94308286; PubMed=7518470;
 RA Hall C.L., Wang C., Lange L.A., Turley E.A.;
 RT "Hyaluronan and the hyaluronan receptor RHAMM promote focal adhesion
 RT turnover and transient tyrosine kinase activity";
 RL J. Cell Biol. 126:575-586(1994).
 RN [7]
 RP ERK REGULATION AND SUBCELLULAR LOCATION.
 RX MEDLINE=98225222; PubMed=9556628;
 RA Zhang S., Chang M.C., Zylka D., Turley S., Harrison R., Turley E.A.;
 RT "The hyaluronan receptor RHAMM regulates extracellular-regulated
 RT kinase";
 RL J. Biol. Chem. 273:11342-11348(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=99059494; PubMed=9845361;
 RA Hofmann M., Assmann V., Fieber C., Sleeman J.P., Moll J., Ponta H.,
 RA Hart I.R., Herrlich P.;
 RT "Problems with RHAMM: a new link between surface adhesion and
 RT oncogenesis";
 RL Cell 95:591-592(1998).
 CC -1- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO
 CC HMMR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE
 CC FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR
 CC TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING
 CC EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY.
 CC -1- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: RHAMM1V4 (SHOWN HERE) AND
 CC RHAMM1. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: URINARY TISSUE EXPRESSED.
 CC
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 CC
 DR EMBL; AF031932; AAC12655.1;
 DR EMBL; AF079222; AAD08670.1;
 DR EMBL; AJ005919; CAA06768.1;
 DR EMBL; AJ005920; CAA06768.1;
 DR EMBL; AJ005921; CAA06768.1; JOINED
 DR EMBL; AJ005922; CAA06768.1; JOINED
 DR EMBL; AJ005923; CAA06768.1; JOINED
 DR EMBL; AJ005924; CAA06768.1; JOINED
 DR EMBL; X64550; CAA45849.1;

RT characterization of the cDNA and chromosomal localization of the gene.
 RT gene: 39:377-384(1997).
 RN [2]
 RC SEQUENCE FROM N.A.
 RA TISSUE-Testis;
 RA MEDLINE=98037449; PubMed=9371398;
 RA Kondoh N., Nishina Y., Tsuchida J., Koga M., Tanaka H., Uchida K.,
 RA Inazawa J., Takeito M., Nozaki M., Nojima H., Matsunaga K., Namiki M.,
 RA Okuyama A., Nishimune Y.,
 RT "Assignment of synaptonemal complex protein 1 (SCP1) to human
 RT chromosome 1p13 by fluorescence in situ hybridization and its
 RT expression in the testis."
 RT Cytogenet. Cell Genet. 78:103-104(1997).
 CC -1- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF
 CC SYNAPTONEMAL COMPLEXES (SCS). FORMED BETWEEN HOMOLOGOUS
 CC CHROMOSOMES DURING MEIOTIC PROPHASE.
 CC -1- SUPRACELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF
 CC SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS.
 CC IS FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS
 CC C-TERMINUS EXTENDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE
 CC SYNAPTONEMAL COMPLEX (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: TESTIS.
 CC -1- DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES,
 CC FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL
 CC DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
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 CC -----
 DR EMBL: X95654; CA64956.1;
 DR EMBL: D67035; BAA2586.1;
 DR Genew: HGNC:11467; STCP1.
 DR MIM: 602162;
 KW Nuclear protein; Meiosis; Cell division; Phosphorylation;
 KW DNA-binding; Coiled coil.
 FT DOMAIN 12 100
 FT DOMAIN 107 798
 FT DOMAIN 117 120
 FT DOMAIN 679 682
 FT DOMAIN 880 883
 FT DOMAIN 961 969
 FT DOMAIN 46 46
 FT CONFLICT 106 106
 FT CONFLICT 153 153
 FT CONFLICT 161 161
 FT CONFLICT 168 168
 FT CONFLICT 216 216
 FT CONFLICT 225 226
 FT CONFLICT 350 350
 FT CONFLICT 360 360
 FT CONFLICT 401 401
 FT CONFLICT 406 406
 FT CONFLICT 415 415
 FT CONFLICT 449 449
 FT CONFLICT 483 510
 FT CONFLICT 516 528
 FT CONFLICT 549 549
 FT CONFLICT 560 560
 FT CONFLICT 805 805
 FT CONFLICT 941 941
 FT CONFLICT 941 941
 FT SEQUENCE 976 AA: 114069 MW: 8BA81D042AC2696B CRC64;
 Query Match 16.0%; Score 191; DB 1; Length 976;
 Best Local Similarity 23.3%; Pred. No. 0.0042;

Matches 79; Conservative 53; Mismatches 103; Indels 104; Gaps 12;
 QY 1 DEKIDSVMSQEDVTAQFESYKALTA---ETEDLK-----TENSISLOKAKAG 47
 Db 402 EDOLKILTMELQKSSSELEEMTKLTNNKEVELEELKVIKGETLTYNNKF-EKIAEL 460
 QY 48 KNAE-----DVQHOILATESSNOEYVRMLDLQTK---SALKETI----- 85
 Db 461 KGTBELGLGLQAREKEVHDLDTLTATTSQYYSKQVNDKTELENEKLTNELTSHC 520
 QY 86 -----KEITVSFLQKITDLONOIKQOEDFRLODEBGRKAKENTTAELTELKMW 138
 Db 521 NKLSLENELT-----QETSDWTLKQOEDINNKKOEERMLKQIENLODETOLNEL 576
 QY 139 RLLEELYNKTRPOTIOLDAF-----VEKQALLNENGAQOEO 177
 Db 577 EYVEELKQKDEVKCKLDSSENCNNLRQVENKKNYIELOQENKALKKGTAEKOL 636
 QY 178 N-----KIRDSYA-----KILGHONLKOKIKHVYKLDENSOLK 211
 Db 637 NVYEIKVKNKLELESQKQFGLTDTYQKEIEDKQISENNLEVEKAKVIADKAVKIQ 696
 QY 212 SEVSKLRQ-----LAKKROSETKLOEELNKYGI 241
 Db 697 KEIDK-RQCKIAEMVALMEKHKHOYDKIIEEDSELGL 734
 RESULT 5
 USOL_YEAST STANDARD; PRT; 1790 AA.
 ID USOL_YEAST
 AC P25386;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Intracellular protein transport protein USOL.
 GN USOL OR INT1 OR YDL058W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180-1A;
 RX MEDLINE=91185402; PubMed=2010462;
 RA Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,
 RA Yamasaki M.,
 RT "A cytoskeleton-related gene, usol, is required for intracellular
 RT protein transport in Saccharomyces cerevisiae."
 RT J. Cell Biol. 113:245-260(1991).
 RN [2]
 RP SEQUENCE OF 782-1790 FROM N.A.
 RA Hostetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N.,
 RA Kendrick K.E.,
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 1-8 FROM N.A.
 RA Bai Y., Symington L.S.,
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR
 CC MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE
 CC ER AND THE GOLGI COMPLEX.
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED
 CC OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL
 CC COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.
 CC -1- SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
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DR EMBL: X53378; CAA38253.1; -

DR EMBL: L03188; AAB00143.1; -

DR EMBL: U53668; AAB66659.1; -

DR PIR: A38455; A38455.

DR SGD: S0002216; USOL.

DR InterPro: IPR002017; Spectrin.

KW Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.

FT DOMAIN 1 726

FT DOMAIN 725 1790

FT DOMAIN 465 1487

FT DOMAIN 991 1790

FT DOMAIN 1172 1786

FT CONFILCT 847 847

FT CONFILCT 924 924

FT CONFILCT 1253 1253

FT CONFILCT 1319 1319

FT CONFILCT 1461 1461

FT CONFILCT 1581 1581

FT CONFILCT 1600 1600

FT CONFILCT 1661 1661

FT CONFILCT 1772 1772

SO SEQUENCE 1790 AA; 206424 MW; 6CE2B216E9FD4818 CRC64;

Query Match 15.5%; Score 185.5; DB 1; Length 1790;

Best Local Similarity 25.3%; Pred. No. 0.015;

Matches 72; Conservative 53; Mismatches 101; Indels 59; Gaps 10;

QY 5 DSMOSLEDTVAQFESYKALITAS-----ETEDKLKLENSLSQEKAKAKNAEDVQHOI 57

DB 1148 ESELEKHEHDLAOLKKEEIOANKEROYNEISQINDEITTSYQOENESIKKKNDELEGV 1207

QY 58 LATESSNOEYVM-----LLDLQTSKAKETKEITV-----SLQKITDLOQL 103

DB 1208 KAKKSTSEOSNLKSEIDLALMLQIKELKKNETEASLESIKSVSETVIKELQDECB 1267

QY 104 KOEDDFRKOLEDGCRKAKENTTAELTEINKRRLYEELYNKTRPQIOLDAF----- 159

DB 1268 NKEKEV--SELEDKLAKSEDKSKYLELOKESK-----IKEELDAITTEIKILOETINIS 1323

QY 160 -----EVE-----KALLNEHGAQEOQLNKIR-----DSYAKLGH-----QNL 193

DB 1324 KAKKSESELRLKTSSEERKNAEOLKELKNEIQIKNOAPEKRRKILNBSSTITQEX 1383

QY 194 KOKIK-----HYVKKLDENSQKSEVSKIRCOLAKKROSETKLOEE 234

DB 1384 SEKITLDELIRLQENELAKKELIDNTRSELEKVSINDELILLE 1428

RESULT 6

MYH4_RABIT

AC 028641: STANDARD: PRT: 1938 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Myosin heavy chain, skeletal muscle, juvenile.

OS Oryctolagus cuniculus (Rabbit).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID:9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-New Zealand white; TISSUE-Skeletal muscle;

RA Maeda K., Hostinova E., Roesch-Kleinhauf A., Schuster H., Gasperik J., Wittinghofer A.;

RT "Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle and a novel cosynthesis of S-1 fragment with the essential and regulatory light chains."

RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: MUSCLE CONTRACTION.

CC -1- SUBUNIT: MUSCLE MYOSTIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE

CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED

CC SUBFRAGMENT (S2).

CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IO DOMAIN.

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CC -----

DR EMBL: U32574; AA74199.1; -

DR HSSP: P13538; 2MYS.

DR InterPro: IPR000048; IO_region.

DR InterPro: IPR004009; Myosin_N.

DR InterPro: IPR002928; Myosin_tail.

DR InterPro: IPR001609; myosin_head.

DR Pfam: PF00063; myosin_head; 1.

DR Pfam: PF00612; IO; 2.

DR Pfam: PF01576; Myosin_tail; 1.

DR Pfam: PF02736; Myosin_N; 1.

DR PRINTS: PR00193; MYOSINHEAVY.

DR ProDom: PD000355; myosin_head; 1.

DR SMART: SM00015; IO; 1.

DR SMART: SM00242; MYSC; 1.

DR PROSITE: PS00096; IO; 1.

DR Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding;

KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;

KW Multigene family.

FT DOMAIN 1 783

FT DOMAIN 784 813

FT DOMAIN 842 1938

FT NP_BIND 179 186

FT DOMAIN 658 680

FT DOMAIN 760 774

FT MOD_RES 35 35

FT MOD_RES 130 130

FT MOD_RES 552 552

FT MOD_RES 756 756

FT MOD_RES 698 698

FT MOD_RES 708 708

SO SEQUENCE 1938 AA; 223064 MW; D8A8A2EC5B182626 CRC64;

Query Match 15.3%; Score 182.5; DB 1; Length 1938;

Best Local Similarity 22.5%; Pred. No. 0.022;

Matches 81; Conservative 54; Mismatches 96; Indels 129; Gaps 13;

QY 8 VOSLEDVTAQFESYKALITASIEDLKLKLENSLSQEKAKAKNAE-----DVHQIILATSS 63

DB 1210 IDNLQVRKQLEKSESLKMEIDL-----ASNMEEVSAKAKGLKMKCTLEQVSELKTK 1265

QY 64 NOEYRMLDLQTSALKETELKEIT-----VSFLQKITDLOQLKQO 106

DB 1266 EEEHQRLLINDSAQRARLQTESGERSROLDKDSIVSOLSRGKAFTQOIEBLKQLEEE 1325

QY 107 -----EED-----FRKQLEDEGGRKAKENTTALTEINKRRLY----- 142

DB 1326 IKAKSALAHAIQSRHDDLLREYEEQEKAKELQGRAMSEVQMRKYETDAIOR 1385

QY 143 -EELYNKTRPQIOLD-----AFVEKQALLNE-----HGAQEOQL 177

DB 1386 TEELSEAKKKRLAQLODAEHEVAVNKKCASLEKTKORLQNEVEDLMIDVERTNAACAL 1445

QY 178 NKIRDSYAKLIG-----HONLKO-----KIKHVVK-----LKDEN 207
 DB 1446 DKORNFDPKILAEWKHEFTAELEASOKESNSTEVEFKVNAVEESIDOLETLKREN 1505
 QY 208 SOKSEVSKIRCOLAR-----KRO-----SETKOELNKVGLK 242
 DB 1506 KNIQREISDLEQIAGGRHIELEKVKQVDEKSELQALAEAEASLEHEGKILRIQ 1565

RESULT 7
 MYH3_RAT
 ID MYH3_RAT STANDARD: PRT: 1940 AA.
 AC P12847;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, fast skeletal muscle, embryonic.
 GN MYH3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP MEDLINE=87060988; PubMed=3783701;
 RA Strehler E.E., Strehler-Page M.-A., Perriard J.C., Perissamy M.,
 Nadal-Ginard B.,
 RT "Complete nucleotide and encoded amino acid sequence of a mammalian
 RT myosin heavy chain gene. Evidence against intron-dependent evolution
 RT of the rod".
 RL J. Mol. Biol. 190:291-317(1986).
 CC -1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATOR LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PFM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC AKTYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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 CC or send an email to license@sib-sib.ch).
 CC EMBL: X04267; CAA27817.1;
 CC PIR: A24922; A24922.
 CC HSSP: P13538; 2MYS.
 CC InterPro: IPR000048; IQ_region.
 CC InterPro: IPR004009; Myosin_N.
 CC InterPro: IPR002928; Myosin_tail.
 CC InterPro: IPR002017; Spectrin.
 CC InterPro: IPR001609; myosin_head.
 CC Pfam: PF00063; myosin_head; 1.
 CC Pfam: PF00612; IQ; 2.
 CC Pfam: PF01576; Myosin_tail; 1.
 CC Pfam: PF02736; Myosin_N; 1.
 CC PRINTS: PR00193; MYOSINHEAVY.
 CC ProDom: PD000355; myosin_head; 1.
 CC SMART: SM00015; IQ; 1.
 CC SMART: SM00242; MYSC; 1.
 DR MYH2_HUMAN STANDARD: PRT: 1941 AA.
 AC Q9URX2; Q16229; Q14322;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, skeletal muscle, adult 2 (Myosin heavy chain IIA)
 DE (MYHC-IIa).
 GN MYH2 OR MYHSA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP MEDLINE=9931869; PubMed=10388558;
 RA Weiss A., Schiaffino S., Leinwand L.A.,
 RT "Comparative sequence analysis of the complete human sarcomeric myosin
 RT heavy chain family: implications for functional diversity".
 RL J. Mol. Biol. 290:61-75(1999).
 RL [2]
 RP SEQUENCE OF 1711-1941 FROM N.A.
 RP TISSUE=Skeletal muscle;
 RC MEDLINE=95109625; PubMed=7545970;
 RA Smerda V., Karsch-Mizrachi I., Campione M., Leinwand L.,
 RA Schiaffino S.,
 RT "Type Iix myosin heavy chain transcripts are expressed in type IIB

DR PROSITE: P650096; IQ; 1.
 KM Myosin: Muscle protein, coiled coil, thick filament; Actin-binding;
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 KW Multigene family.
 FT DOMAIN 1 781 MYOSIN HEAD-LIKE.
 FT DOMAIN 782 811 COILED COIL (POTENTIAL).
 FT DOMAIN 840 1933 ATP (POTENTIAL).
 FT NP_BIND 179 186 ACTIN-BINDING.
 FT DOMAIN 656 678 ACTIN-BINDING.
 FT MOD_RES 758 772 METHYLATION (TR1-) (POTENTIAL).
 FT MOD_RES 130 130 METHYLATION (SH-1).
 FT MOD_RES 696 696 ALKYLATION (SH-2).
 FT MOD_RES 706 706 ALKYLATION (SH-2).
 SQ SEQUENCE 1940 AA; 223857 MW; B5D546A5965696 CRC64;

Query Match 15.28; Score 181.5; DB 1; Length 1940;
 Best Local Similarity 19.48; Pred. No. 0.025;
 Matches 69; Conservative 62; Mismatches 104; Indels 121; Gaps 7;

QY 8 VQSLDYTAQFESYKALTAETEDLKLNSLOEKAKKAKNMDVGHOLATESSNOET 67
 DB 1208 IDNLQVKKLEKSEFKLEIDLSSVSASVSKSKANLEKICRTLEDQLEARGKNEET 1267
 QY 68 VRMLDIQTSALKETREKIT-----VSFLQKITDLONLQOQED- 109
 DB 1268 QRSLSLTTQKSRLOTEGELSLRLEEKESIVQSLSQAFYQQLIEELKRLQLEENKAK 1327
 QY 110 FRKQLEDEGRKAKETTELLEIKMKRLVE----- 143
 DB 1328 MALAHLOSSRHCCLRLREYEEQEGKALQALSKANSEVQMTKYETDAIQTEEL 1387
 QY 144 ELYN-----KTR----- 150
 DB 1388 EEAQKLAQRLDSEQVEAVNKAQSLKTKRQLOGEVDMADVERANSIAALAKRKQ 1447
 QY 151 PEOIOLAEFEVKQALNHEGAEOQLNKIRDSYAKLIG-----HONLK 194
 DB 1448 RNDKVLAEWKRCESQAELEAKESRSLSTLEFKLNAVEALDQLETKYRKKNLE 1507
 QY 195 QKIKHVVKLKDENSEQSKSEVSKIRCOLAKK-----QSETKLOELNKVGLK 242
 DB 1508 QELADLTQIAGNGKIHLEKSKROMLEKADIQMALEAEALAEHEBAKILRIQ 1563

RESULT 8
 MYH2_HUMAN STANDARD: PRT: 1941 AA.
 AC Q9URX2; Q16229; Q14322;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, skeletal muscle, adult 2 (Myosin heavy chain IIA)
 DE (MYHC-IIa).
 GN MYH2 OR MYHSA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP MEDLINE=9931869; PubMed=10388558;
 RA Weiss A., Schiaffino S., Leinwand L.A.,
 RT "Comparative sequence analysis of the complete human sarcomeric myosin
 RT heavy chain family: implications for functional diversity".
 RL J. Mol. Biol. 290:61-75(1999).
 RL [2]
 RP SEQUENCE OF 1711-1941 FROM N.A.
 RP TISSUE=Skeletal muscle;
 RC MEDLINE=95109625; PubMed=7545970;
 RA Smerda V., Karsch-Mizrachi I., Campione M., Leinwand L.,
 RA Schiaffino S.,
 RT "Type Iix myosin heavy chain transcripts are expressed in type IIB

RT Fibers of human skeletal muscle.";
 RL Am. J. Physiol. 267:C1723-C1728(1994);
 RN [3]
 RP SEQUENCE OF 1823-1941 FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA MEDLINE-95270723; PubMed-7751403;
 RX Enlioni S., Sant'ana Pereira J., Sargeant T., Young A., Goldspink G.;
 RT "Characterization of human skeletal muscle fibres according to the
 RT myosin heavy chains they express.";
 RL J. Muscle Res. Cell Motil. 16:35-43(1995).
 CC -1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LMW) AND 1 HEAVY MEROMYOSIN (HMW). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
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 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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 CC
 DR EMBL: AF11784; AB229950.1;
 DR EMBL: S73840; AAC13916.1;
 DR EMBL: Z32858; CAA83687.1;
 DR HSSP: P13538; 2MYS.
 DR Genew: HGNC:7572; MYH2.
 DR MIM: 160740;
 DR InterPro: IPR000048; IQ_region.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR001609; myosin_head.
 DR Pfam: PF00063; myosin_head.
 DR Pfam: PF00612; IQ_2.
 DR Pfam: PF01576; Myosin_tail.
 DR Pfam: PF02736; Myosin_N_1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ_1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ_1.
 DR Myosin_Muscle_protein; Coiled coil; Thick filament; Actin-binding;
 DR Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 DR Multigene family;
 FT DOMAIN 1 786 MYOSIN HEAD-LIKE.
 FT DOMAIN 787 816 IQ.
 FT DOMAIN 845 1941 COILED COIL (POTENTIAL).
 FT NP_BIND 179 186 ATP (POTENTIAL).
 FT CONFLICT 1844 1844 K -> R (IN REF. 3).
 SQ SEQUENCE 1941 AA; 223043 MW; 681E866F83AEAB3F CRC64;
 Query Match 15.1%; Score 180.5; DB 1; Length 1941;
 Best Local Similarity 24.2%; Pred. No. 0.028;
 Matches 87; Conservative 50; Mismatches 94; Indels 129; Gaps 15;
 QY 8 VOSLDVTAOFESYKALATSEDEKLKLNSSLOEKAARKNAE-----DVQHQLATSS 63
 DB 1213 IDNLRVQKLEKESEKMEIDL-----ASVVEVSKAKGKMKRTLEQSLSEKSK 1268.
 QY 64 NOEYRMALD-----LQTKSA--LKETEKEITVS-----FLQKITDLONLKQO 106

Db 1269 EEEQRLINLTLAQRGLQRESSEFSRQIDKEKALVSQSRGKAFTQQLBELKROLEE 1328
 QY 107 -----EED---FKOLEDEGRKAKEKNTVTELEIKMKRLY----- 142
 Db 1329 IKAKNALAHALOSSRHCDLLREQYEDESESKAEIQLSKAMTEVAVQMKRTETDAIOR 1388
 QY 143 -EELYNKTRKPFQIOLDA-----FEVERKALNE-----HGAQEQ 117
 Db 1389 TEELFEKKTLAQRQAEEHVEVNAKCKASLEKTKORLQNEVEDMLDYERTNAACAL 1448
 QY 178 NKTRDSYAKLLG-----HONLKO-----KIKHYK-----LKDN 207
 Db 1449 DKQQRNDRKILAEWKQCEFTHALEASQKEARSLGTFLPKIKNAVEESLDQLETKREN 1508
 QY 208 SOLKSESKIRQOLAK-----KKO-----SETKLOELNKYVGIK 242
 Db 1509 KNLQOEISDLTEQIAEGKRRIHELEKIKQVEQKCELAQALBEAEASLEHEEGKILRIQ 1568
 RESULT 9
 ID MYSS_CHICK STANDARD; PRT; 1938 AA.
 AC P13538; 013228;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, skeletal muscle, adult.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Pectoralis muscle;
 RA Chao T.H., Bandman E., Moore L.;
 RT "Cloning, nucleotide sequence and characterization of a full-length
 RT cDNA encoding the myosin heavy chain from adult chicken pectoralis
 RT major muscle.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-205.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE-92041767; PubMed-1939027;
 RA Hayashida M., Maeta T., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: I.
 RT Sequence of the amino-terminal 23 kDa fragment.";
 RL J. Biochem. 110:54-59(1991).
 RN [3]
 RP SEQUENCE OF 206-636.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE-92041768; PubMed-1939028;
 RA Komine Y., Maeta T., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: II.
 RT Sequence of the 50 kDa fragment of subfragment-1.";
 RL J. Biochem. 110:60-67(1991).
 RN [4]
 RP SEQUENCE OF 637-837.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE-92041769; PubMed-1939029;
 RA Maeta T., Miyajishi T., Matsuzono K., Tanioka Y., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: III.
 RT Sequence of the 22 kDa fragment and the alignment of the 23 kDa, 50
 RT kDa, and 22 kDa fragments.";
 RL J. Biochem. 110:68-74(1991).
 RN [5]
 RP SEQUENCE OF 838-1938.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE-92041770; PubMed-1939030;
 RA Maeta T., Yajima E., Nagata S., Miyajishi T., Nakayama S., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: IV.
 RT Sequence of the rod, and the complete 1,938-residue sequence of the

RT heavy chain.";
 RN J. Biochem. 110:75-87(1991).
 [6]
 RP PRELIMINARY SEQUENCE OF 1-808
 RX MEDLINE=87092420; PubMed=3467365;
 RA Maita T., Hayashida M., Tanioka Y., Komine Y., Matsuda G.,
 RT "The primary structure of the myosin head.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:416-420(1987).
 RN [17]
 RP SEQUENCE OF 842-1270.
 RX MEDLINE=90121764; PubMed=2610940;
 RA Watanabe B.;
 RT "Complete amino-acid sequence of subfragment-2 in adult chicken
 RL Biol. Chem. Hoppe-Seyler 370:1027-1034(1989).
 RN [18]
 RP SEQUENCE OF 852-1108.
 RX MEDLINE=89374803; PubMed=2775482;
 RA Watanabe B.;
 RT "Amino-acid sequence of the short subfragment-2 in adult chicken
 RL Biol. Chem. Hoppe-Seyler 370:549-558(1989).
 RN [19]
 RP SEQUENCE OF 1145-1270.
 RX MEDLINE=89228549; PubMed=2713098;
 RA Watanabe B.;
 RT "Amino-acid sequence of the hinge region in chicken myosin
 RL Biol. Chem. Hoppe-Seyler 370:55-61(1989).
 RN [10]
 RP SEQUENCE OF 1857-1938 FROM N.A.
 RX MEDLINE=87217964; PubMed=3034534;
 RA Moriarty D.M., Barringer K.J., Dodgson J.B., Richter H.E.,
 RT "Genomic clones encoding chicken myosin heavy-chain genes.";
 RL DNA 6:91-99(1987).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1-843.
 RX MEDLINE=93303624; PubMed=8316857;
 RA Rayment I., Rypniewski W.R., Schmidt-Base K., Smith R.,
 RA Tomchick D.R., Bennett M.W., Winkelmann D.A., Wesenberg G.,
 RT "Three-dimensional structure of myosin subfragment-1: a molecular
 motor.";
 RL Science 261:50-58(1993).
 RN [1]
 RP F-ACTIN AND HAS ATPASE ACTIVITY. MYOSIN IS A PROTEIN THAT BINDS TO
 CC -1- SUBUNIT. MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC -1- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPEITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUPERFRAGMENT (S2).
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 TO DOMAIN.
 CC
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 CC
 CC EMBL; U07231; AAB47555.1;
 CC DB; M16557; AAA48970.1;

DR	PIR: PX0050; PX0051.	
DR	PIR: A26821; A26821.	
DR	PIR: S02082; S02082.	
DR	PIR: S04501; S04501.	
DR	PIR: S05515; S05515.	
DR	PDB: 2MTS; 1J-JAN-97.	
DR	InterPro: IPR000048; IO_region.	
DR	InterPro: IPR004009; Myosin_N.	
DR	InterPro: IPR002928; Myosin_tail.	
DR	InterPro: IPR001609; myosin_head.	
DR	Pfam: PF00063; myosin_head.1.	
DR	Pfam: PF00612; IO: 2.	
DR	Pfam: PF01576; Myosin_tail.1.	
DR	Pfam: PF02736; Myosin_N.1.	
DR	ProDom: PD000355; myosin_head.1.	
DR	SMART; SM00015; IO: 1.	
DR	SMART; SM00242; MYSC; 1.	
DR	PROSITE; PS50096; IO: 1.	
KW	Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;	
KW	ATP-binding; Methylation; Alkylation; Phosphorylation; Acetylation;	
KW	Calmodulin-binding; Multigene family; 3D-structure.	
FT	INIT_MET 0	
FT	DOMAIN 1 782	MYOSIN HEAD-LIKE.
FT	DOMAIN 783 812	IO.
FT	DOMAIN 838 840	HINGE.
FT	DOMAIN 841 1938	COILED COIL (POTENTIAL).
FT	NP_BIND 179	ATP (POTENTIAL).
FT	DOMAIN 657 679	ACTIN-BINDING.
FT	MOD_RES 739	ACTIN-BINDING.
FT	MOD_RES 1	ACETYLATION.
FT	MOD_RES 35	METHYLATION (MONO-).
FT	MOD_RES 130	METHYLATION (TRI-).
FT	MOD_RES 551	METHYLATION (TRI-).
FT	MOD_RES 755	METHYLATION (MONO-).
FT	MOD_RES 697	METHYLATION (MONO-).
FT	MOD_RES 707	ALKYLATION (SH-1).
FT	CONFLICT 907 907	ALKYLATION (SH-1).
FT	CONFLICT 980 980	C->Q (IN REF. 7 AND 8).
FT	CONFLICT 1343 1343	L->F (IN REF. 1).
FT	CONFLICT 1545 1545	E->D (IN REF. 5).
FT	CONFLICT 1796 1797	S->A (IN REF. 5).
FT	CONFLICT 1830 1830	HV->QL (IN REF. 5).
FT	CONFLICT 1863 1863	S->A (IN REF. 5).
FT	CONFLICT 1929 1931	I->V (IN REF. 10).
FT	CONFLICT 1938 1938	IHG->FH (IN REF. 10).
FT	SEQUENCE 1938 AA; 223013 MW; EDD01CAA2681E10F CRC64;	
Query Match	15.0%; Score 179.5; DB 1; Length 1938;	
Best Local Similarity	20.5%; Pred. No. 0.032;	
Matches	73; Conservative 55; Mismatches 107; Indels 121; Gaps 9;	
OY	8 VOSLEDVYAOFEESKALTASEIEDLKENSLOEKAKKAGNAEDVOHOLATNESSNOEX 67	
DB	1209 IDNLOVKOKLEKESKSLKNEIDLASNMESVSKANAEKMCRTLEDOLSEIKTEEON 1268	
OY	68 VRMLDLOTSALKETBEI-----KETTVS-----FLQRTDLONLKOE 107	
DB	1269 ORNINDLNTORALQLOETGETYSROAEKDALISQLSRGKGFQOIEELKRLHEEIRAK 1328	
OY	108 -----EPRKOLEDEGRKAEKETTALTEELINKRWLY-----EEL 145	
DB	1329 MALAHAGSARHDCCLLRQYEEOAKGELORALSKANSEVAOWRTYEEDALQRTTEL 1388	
OY	146 YNKTREFQOLD-----AEVEQOALINE-----HGAAGQOLNKR 181	
DB	1389 EERKKLQARLODAEHEEAVANAKCASLEKTKORLQNEVEDLMDVENSNAACALDKQ 1448	
OY	182 DSYAKLGHONLK-----OKIHVYKLKDNESQK 211	
DB	1449 KNEFDILAEKQKYEETOTELBASOKESRSLSLETFKKNAYEESLDHLFTLREKNK 1508	
OY	212 SEVSKLRQOLA-----RK-----KQSEPTLOELNKKVIGIK 242	
DB	1509 QEIDLTFOILAEGGKAVAELEKVKKHVQEKSELQASLEAEASLEHEEKGKILRIQ 1564	


```

SQ SEQUENCE 1939 AA; 223012 MW; 40BLADID777A47DE CRC64;

Query Match      15.0%; Score 179.5; DB 1: Length 1939;
Best Local Similarity 18.7%; Pred. No. 0.032;
Matches 67; Conservative 61; Mismatches 104; Indels 127; Gaps 7;

OY 8 VQSLIEDVTAQEESYKALFASIEEDLKLNSLSLOEAKKAGKAENADVOHQIATLESSNOEY 67
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 121 IDSLOARKQKLEKEKSELKMEINDLASNMETVSRAKANFEKMCRTLEDQLSEIKTEEEQ 1270
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
OY 68 VRMLDLOTKSALKETEIKEIT-----VSFLQKITDILOQLKOGEED- 109
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 1271 QRLNELSNAQKARLHTSGESGRDLDEKDANVSOLSKQAFPTQIEELKQLEETRYAK 1330
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
OY 110 -----FRKODEEGRKAENEKNTTAELETBEINKRWLLYE----- 143
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 1331 STLHALQSARHDDDLLREQYEEBQEPAAKIELQRMKSANSVEVAQMRTKYEFDAIQTEEL 1390
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
OY 144 -----ELYNKTKPFOIQL----- 156
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 1391 EEAKKKLAQRLODAEEHVEAVNSCASLEKTKORLQEOVEDLMIDEVSRNACIALDKQ 1450
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
OY 157 -----DAFVEVKQALLNEGQAQDELNTIRDSYAKULLGH-----QNLK 194
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 1451 RNEDKVLAEMKQKEYETQALEASOKRSRSTLETFVKNKNYSLDHLTLTKRENKNLQ 1510
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
OY 195 QKI-----KHVVKLKDEMSOLSKSEVSKLRCLAKKQOSEFYKLOEELNVLGIRK 242
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 1511 QEISDLNEQAEGKHIHELEKVKAKOLDHEKSELQTSL---EAMVASLHEHGKILRIQ 1566
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 11
MFPI_LYCSES STANDARD: PRT; 697 AA.
AC AC MFPI_LYCSES 697 AA.
AC P93203:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MAR binding filament-like protein 1.
DE GN MFPI.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VENT Cherry; TISSUE=Fruit;
RX MEDLINE=97112038; PubMed=8953774;
RA Meier I., Phelan T., Grussem W., Spiker S., Schneider D.;
RT "MFPI, a novel plant filament-like protein with affinity for matrix
attachment region DNA.";
RL Plant Cell 8:2105-2115(1996).
CC CC -FUNCTION: BINDS DNA. INTERACTS WITH CHROMATIN VIA MATRIX
ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NUCLEAR
ARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR MATRIX AND
POTENTIALLY WITH THE NUCLEAR ENVELOPE.
CC CC -SUBCELLULAR LOCATION: NUCLEAR MATRIX.
CC CC -----
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb.ch/announce/
or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL; Y07861; CAA69181.1; .
KW Nuclear protein; DNA-binding; Coiled coil.
FT DOMAIN 125 681 COILED COIL (POTENTIAL).
FT POLY-SER. 10 15
SQ SEQUENCE 697 AA; 79516 MW; 700A556D86DA7E49 CRC64;
```

Query Match 15.0%; Score 179; DB 1; Length 697;
 Best Local Similarity 25.6%; Pred. No. 0.012;
 Matches 72; Conservative 57; Mismatches 96; Indels 56; Gaps 12;

QY 1 QEKDSWQSLQEDVTAQFESKALTAS---EIEDIKLENSLSQEKAKAGNAEDVQH--55
 DB 427 QESLENSRSEVSDITVQLEQRLDSKLEKREVSQKQME---LEEFRASTQNRIDETKISS 483
 QY 56 QILATE-----SSNOEYVRMLDQTSALKETFKITVYSFLQKITDLQNOKQO 106
 DB 484 ELALAEITTTKELLKLTNEEHNTMSDELAVSENRSDLOTEL-VNYYKREHTRNELKOE 542
 QY 107 -----EEDFRKQLEDEGRKAKEENTTALETETINKMRL-LVEEL 145
 DB 543 KTVITTELEELKFLQESQTRKEKRLSLEDE---LEE---ATSLDEINNVALLAEEL 595
 QY 146 YNKTTPQIQLDAEVEKQALLNEHGAQEQLNKIRPSYAKL-----GHOMKQKIRHYV 201
 DB 596 ELATSRNSLSEDEREVRHRSQSEKQISQEQNELEDAHSIVMLGKERESLEKRAK---652
 QY 202 KLEDENSQLSEVSKLRQCLAKKQSETKLOEELNKVGLGR 242
 DB 653 KLEDEMAAKGEILRLRSQINSVK---APVEDEKVVAGGEK 690.

RESULT 12
 MYHL_HUMAN STANDARD; PRT; 1939 AA.
 ID MYHL_HUMAN
 AC P12882; Q9Y622;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, skeletal muscle, adult 1 (Myosin heavy chain
 Iix/d) (MyHC-Iix/d).
 GN MYH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA MEDLINE=99318659; PubMed=10388558;
 RX Weiss A., Schiaffino S., Leinwand L.A.;
 RT "Comparative sequence analysis of the complete human sarcomeric myosin
 heavy chain family: implications for functional diversity.";
 RL J. Mol. Biol. 290:61-75(1999).
 RN [2]
 RP SEQUENCE OF 1064-1939 FROM N.A.
 RX MEDLINE=66176778; PubMed=2421254;
 RA Saez L., Leinwand L.A.;
 RT "Characterization of diverse forms of myosin heavy chain expressed in
 adult human skeletal muscle.";
 RL Nucleic Acids Res. 14:2951-2969(1986).
 CC 1- FUNCTION: MUSCLE CONTRACTION.
 CC 1- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC 1- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
 CC 1- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC 1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC 1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 MEROMYOSIN (LMH) AND 1 HEAVY MEROMYOSIN (HMH). IT CAN LATER BE
 SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 SUBFRAGMENT (S2).
 CC 1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC 1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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 or send an email to license@sib-sib.ch).

CC EMBL; AF111785; AAD29951.1;
 CC EMBL; X03740; CAA27380.1;
 CC PIR; A23767; A23767.
 CC HSSP; P13538; 2MYS.
 CC Genew; HGNC:7567; MYH1.
 CC MIM: 160730;
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR004009; Myosin_N.
 DR InterPro; IPR002928; Myosin_tail.
 DR InterPro; IPR001609; myosin_head.
 DR Pfam; PF00063; myosin_head_1.
 DR Pfam; PF00612; IQ_2.
 DR Pfam; PF01576; Myosin_tail_1.
 DR Pfam; PF02736; Myosin_N_1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD000355; myosin_head_1.
 DR SMART; SM00015; IQ_1.
 DR SMART; SM00242; MYSC_1.
 DR PROSITE; PS50096; IQ_1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 KW Multigene family.
 FT FT DOMAIN 1 784
 FT FT 785 814
 FT FT 815 843
 FT FT 844 861
 FT FT NP_BIND 179 186
 FT FT 187 193
 FT FT DOMAIN 659 681
 FT FT 682 755
 FT FT 756 775
 FT FT MOD_RES 130 130
 FT FT 131 130
 FT FT MOD_RES 699 699
 FT FT 700 709
 FT FT 710 709
 FT FT 710 1131
 FT FT 1132 1139
 FT FT 1140 1158
 FT FT 1159 1163
 FT FT 1164 1289
 FT FT 1290 1303
 FT FT 1304 1451
 FT FT 1452 1451
 FT FT 1452 1470
 FT FT 1471 1470
 FT FT 1471 1473
 FT FT 1474 1569
 FT FT 1570 1569
 FT FT 1570 1598
 FT FT 1599 1606
 FT FT 1607 1606
 FT FT 1607 1643
 FT FT 1644 1648
 FT FT 1649 1750
 FT FT 1751 1822
 FT FT 1823 1845
 FT FT 1846 1845
 SO SEQUENCE 1939 AA; 223114 MW; 39AD26AB790FA53 CRC64;

Query Match 14.9%; Score 178.5; DB 1; Length 1939;
 Best Local Similarity 23.3%; Pred. No. 0.036;
 Matches 84; Conservative 51; Mismatches 96; Indels 129; Gaps 14;

QY 8 VQSLQEDVTAQFESKALTASSETIEDIKLENSLSQEKAKAGNAED---VQHQILATSS 63
 DB 1211 IDNLRVQKQLEKRESEKMEKEDIDL---ASNMETVSKAKGMLEKCRALQELQSEIKTK 1266
 QY 64 NOEYVRMLDQTSALKETETI-----KEIVYS-----FLOKITDLONOKQO 106
 DB 1267 EEEQQRLLINDLAQARARLQTESGEYSRQLEKQDITVLSQSRKQAFQOIEELKQLESE 1326
 QY 107 -----EED---FKQLEDEGRKAKEENTTALETETINKMRLY-----142
 DB 1327 IKAKSALAHALQSSRHDDQLREQYEEQDEAALQDRMSKNSSEVAQWRTYETDAIOR 1386
 QY 143 -EELYNKTRKPPQIQD-----AFVEKQALLNE-----HGAAGQQL 177

Db 1387 TEELEKKKLAORLQDAEHEVAVNAKCAASLEKTKORLONEVEDIMIDVERTNAACAAL 1446
 QY 178 NKTRDSYAKLLG-----HONLKO-----KIRHYV-----LKDN 207
 Db 1447 DKQORNFDKLAEWKOKCEETHAELEPSOKESLSLETKIRNANEESIDQLETKREN 1506
 QY 208 SOLKSEVSKLRQCLAR-----KKO-----SETKLOEELNKVLGIR 242
 Db 1507 KNQOETSDLEQIAEGGKRIHELEKIKKQVEKESRLQALAEAEASLEHEGKILIRIQ 1566
 RESULT 13
 MYH3_HUMAN STANDARD; PRT; 1940 AA.
 ID MYH3_HUMAN
 AC P11055; Q15492; (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, fast skeletal muscle, embryonic (muscle embryonic
 DE myosin heavy chain) (SMCE).
 GN MYH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89263803; PubMed=2726495;
 RA Eller M.S., Steadman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,
 RA Rubinstein N.A., Kelly A.M., Sarkar S.;
 RT "Nucleotide sequence of full length human embryonic myosin heavy
 RT chain cDNA.";
 RL Nucleic Acids Res. 17:3591-3592(1989).
 RN [2]
 RP SEQUENCE OF 774-1940 FROM N.A.
 RA MEDLINE=90033298; PubMed=2806546;
 RA Eller M.S., Steadman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,
 RA Raychowdhury M.K., Rubinstein N.A., Kelly A.M., Sarkar S.;
 RT "Human embryonic myosin heavy chain cDNA. Interspecies sequence
 RT conservation of the myosin rod, chromosomal locus and isoform
 RT specific transcription of the gene.";
 RL FEBS Lett. 256:21-28(1989).
 RN [3]
 RP SEQUENCE OF 856-1940 FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA MEDLINE=90235862; PubMed=1691980;
 RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
 RA Arnold H.H.;
 RT "Identification of three developmentally controlled isoforms of human
 RT myosin heavy chains.";
 RL Eur. J. Biochem. 189:55-65(1990).
 RN [4]
 RP SEQUENCE OF 856-1940 FROM N.A.
 RA MEDLINE=89366648; PubMed=2771643;
 RA Karsch-Mizrachi I., Travis M., Bleu H., Leitwand L.A.;
 RT "Expression and DNA sequence analysis of a human embryonic skeletal
 RT muscle myosin heavy chain gene.";
 RL Nucleic Acids Res. 17:6167-6179(1989).
 CC -1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC -1- DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL MUSCLE
 CC AND NOT PRESENT OR BARELY DETECTABLE IN HEART AND ADULT SKELETAL
 CC MUSCLE.
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC AKTYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MEROMYOSIN (LMN) AND 1 HEAVY MEROMYOSIN (HMN). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: X13988; CA332167.1;
 CC EMBL: X13100; CA331492.1;
 CC EMBL: X51593; CA335942.1;
 CC EMBL: X15696; CA333731.1;
 CC PIR: S04090; S04090.
 CC HSP: P13538; 2MYS.
 CC Genew: HGNC:7573; MYH3.
 CC MIM: 160720;
 CC InterPro: IPR000048; IQ_region.
 CC InterPro: IPR004009; Myosin_N.
 CC InterPro: IPR002928; Myosin_tail.
 CC InterPro: IPR001609; myosin_head.
 CC Pfam: PF00063; myosin_head; 1.
 CC Pfam: PF00612; IQ; 2.
 CC Pfam: PF01576; Myosin_tail; 1.
 CC Pfam: PF02736; Myosin_N; 1.
 CC PRINTS: PR00193; MYOSINHEAVY.
 CC ProDom: PD000355; myosin_head; 1.
 CC SMART: SM00015; IQ; 1.
 CC SMART: SM00242; MYSC; 1.
 CC PROSITE: PS50096; IQ; 1.
 CC Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 CC Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 CC Multigene family.
 CC
 CC FT DOMAIN 1 781 MYOSIN HEAD-LIKE.
 CC FT DOMAIN 840 811 IQ.
 CC FT NP_BIND 179 186 COILED COIL (POTENTIAL).
 CC FT DOMAIN 656 678 ATP (POTENTIAL).
 CC FT DOMAIN 758 772 ACTIN-BINDING.
 CC FT MOD_RES 130 130 METHYLATION (TR-) (POTENTIAL).
 CC FT MOD_RES 696 696 ALKYLATION (SH-1).
 CC FT MOD_RES 706 706 ALKYLATION (SH-2).
 CC FT CONFLICT 1331 1331 A -> G (IN REF. 3).
 CC FT CONFLICT 1391 1392 KK -> QE (IN REF. 1 AND 2).
 CC FT CONFLICT 1608 1609 SR -> RA (IN REF. 3).
 CC FT CONFLICT 1663 1664 RG -> QT (IN REF. 2).
 CC SQ SEQUENCE 1940 AA; 224035 MW; 43CA58C6A4BA1253 CRC64;
 CC
 CC Query Match 14.9%; Score 178.5; DB 1; Length 1940;
 CC Best Local Similarity 19.1%; Pred. No. 0.036;
 CC Matches 68; Conservative 62; Mismatches 105; Indels 121; Gaps 7;
 CC
 CC QY 8 VQSLDYVTPQFESYATLRTSEIEDLKLNSIQEKAARKGAEDVQHOIATNESSNOEY 67
 CC Db 1208 IDNLRVQKLEKESEFKLEIDLSSMSYSKSKANLEKICRTLEQDLSBARKNEBI 1267
 CC QY 68 VMLDLQTSKALKEIKETI-----VSLQKITDQNLQKQOED- 109
 CC Db 1268 QRSLSLTQKSRLOTEGELSRQLEKESIVQSRSKQATPQOOTEELKRLQLEENKAK 1327
 CC QY 110 -----FKRLQDEGRKRAKENTTAELTEINKRRLYE- 143
 CC Db 1328 NALAHALQSRHDCDLRLQVQEEBQKAEQLQALSKANSEVAQKRTYETAIOITEEL 1387
 CC QY 144 -----ELYN-----KTK----- 150
 CC Db 1388 EEAKKKLAORLQDSEQVEAVNAKCAASLEKTKORLQGEVEDLMVVERANSIAALDKKO 1447

QY 151 -----PROIOLDAFEVEKQALLNEHGAOEOJLNKIDRSYAKLIG-----HONIK 194
 DB 1448 RNDKVLAEKKTKCESSQAELESLKESRSLSTELKLNKNAVEALDOLETYREKNKIE 1507
 QY 195 QKIKHVYKLDKENSQKSESKLRQOLAKK-----QSEKLOEELNKVYLGK 242
 DB 1508 QETADLTQIAENGKTHHELEKSRKOIELEKADIOALDEAEALAEHEBKILRIO 1563

RESULT 14

SCPL_MESAU STANDARD: PRT: 845 AA.
 ID SCPL_MESAU 060563:
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Synaptonemal complex protein 1 (SCP-1 protein) (Meiotic chromosome synaptonemal complex protein 1 (SCP-1 protein) (Fragment)).
 DE Synaptonemal complex protein 1 (SCP-1 protein) (Meiotic chromosome synaptonemal complex protein 1 (SCP-1 protein) (Fragment)).
 GN SCPL OR STN1.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=95181577; PubMed=7876143;
 RA Dobson M.J., Pearlman R.E., Karatsakis A., Spyropoulos B., Moens P.B.,
 "Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disjunction."
 RL J. Cell Sci. 107:2749-2760(1994)
 CC -1- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS CHROMOSOMES DURING MEIOTIC PROPHASE (BY SIMILARITY). HAS NON-SPECIFIC DNA BINDING CAPABILITY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS. FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE SYNAPTONEMAL COMPLEX.
 CC -1- DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES, FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
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 CC EMBL, I32978; AAC2039.1;
 DR Nuclear protein; Meiosis; Cell division; Phosphorylation;
 KW DNA-binding; Coiled coil.
 FT NON-TER 1
 FT DOMAIN <1 672 COILED COIL (POTENTIAL).
 FT DOMAIN 553 556 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 753 756 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 830 838 ARG/LYS-RICH (BASIC).
 SO SEQUENCE 845 AA; 99401 MW; DFE28873C824C6A8 CnC64;

Query Match 14.8%; Score 176.5; DB 1; Length 845;
 Best Local Similarity 23.1%; Pred. NO. 0.02;
 Matches 79; Conservative 55; Mismatches 97; Indels 111; Gaps 14;

QY 5 DSMVOSLEDVYAOEFYKALATSEIEJLKNSSLO-EKAK--AGKNAR-----51
 DB 273 DEMTKFNNNEVKLEELKTLIA---EDOKLDEKKYKAELEELQGEQETLLLOTRK 329

QY 52 ----DVQHOILATNESSNOEYVRLDLQTRSAKETEIR--ETVS-----FLOKI 96
 DB 330 EVDHLEEOILVYTKISDQNSKQVEELKIR--LEEEKLNAAELTACGSLSENKLTQET 387
 QY 97 TDLOAOL-----KQOEEDFKQLEDEGR-----120
 DB 388 NDMALELKRYOBDITNSKQOEERMLKQTEENLEEKETHRDELESYRKEFFIOGNEVCKL 447
 QY 121 -----KAER-----ENTTAELTEELNKRLLYEELYNKTRPQ-----153
 DB 448 DKSEENARSICEVYLKKEKQKILKNCNNRKAQENKSKYIEELHODENALAKKSSAES 507
 QY 154 IQLAEFEVEKQALLNEHGAOEOJLNKIDRSY-----AKLIGHQMLKQIKHVYKLDKENS 208
 DB 508 KQLNAYELKVKLQLELESAAKQKQEMTDNYQKEIEVKKISEEKLGLVEKAKMVDVAV 567
 QY 209 QLKSEVSKLRQO-----LARKQSEFKLOELNKVYGI 241
 DB 568 KLRKEID-LRQGHIAEMVAMEKHKQYDIYVEERSEJGL 608

RESULT 15

MYH8_HUMAN STANDARD: PRT: 1937 AA.
 ID MYH8_HUMAN P13535; Q14910;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Myosin heavy chain, skeletal muscle, perinatal (MyHC-perinatal).
 GN MYH8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=90323631; PubMed=2373371;
 RA Karsch-Mizrachi I., Peghaili R., Shows T.B. Jr., Leinwand L.A.;
 RT "Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA."
 RL Gene 89:289-294(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=95324556; PubMed=7601129;
 RA Julian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S., Stegman H.H., Rubinstein N.A.;
 RT "Characterization of a human perinatal myosin heavy-chain transcript."
 RL Eur. J. Biochem. 230:1001-1006(1995).
 RN [3]
 RP SEQUENCE OF 502-1937 FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=90235862; PubMed=1691980;
 RA Robert E., Buchberger-Seidl A., Braun T., Singh S., Goede H.W., Arnold H.H.;
 RT "Identification of three developmentally controlled isoforms of human myosin heavy chains."
 RL Eur. J. Biochem. 189:55-65(1990).
 RN [4]
 RP SEQUENCE OF 860-1937 FROM N.A.
 RX MEDLINE=89234168; PubMed=2715179;
 RA Peghaili R., Leinwand L.A.;
 RT "Molecular genetic characterization of a developmentally regulated human perinatal myosin heavy chain."
 RL J. Cell Biol. 108:1791-1797(1989).
 RN [5]
 RP SEQUENCE OF 1-46 FROM N.A.
 RA Esser K., Tidhar A., Myszkowski M.;
 RT "Isolation and characterization of the human perinatal MHC promoter."
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBD databases.
 CC -1- FUNCTION: MUSCLE CONTRACTION.

CC 1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC 1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC 1- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC 1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC SUBFRAGMENT (S2).
CC 1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC 1- SIMILARITY: CONTAINS 1 IO DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: M36769; AAC17185.1; -
DR EMBL: Z38133; CAA86293.1; -
DR EMBL: X51592; CAA35941.1; -
DR EMBL: AF067143; AAC21557.1; -
DR PIR: A30220; A30220.
DR HSSP: P13538; 2MTS.
DR GeneW: HGNC:7578; MYH8.
DR MIM: 160741; -
DR InterPro: IPR000048; IO_region.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF00612; IO; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IO; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IO; 1.
DR Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW ATP-binding; Methylation; Alkylation; Multigene family;
KW Calmodulin-binding.
FT DOMAIN 1 780 MYOSIN HEAD-LIKE.
FT DOMAIN 1 813 IO.
FT DOMAIN 842 1937 COILED COIL (POTENTIAL).
FT NP_BIND 181 188 ATP.
FT DOMAIN 658 680 ACTIN-BINDING.
FT DOMAIN 760 774 ACTIN-BINDING.
FT MOD_RES 132 132 METHYLATION (TR1-) (POTENTIAL).
FT MOD_RES 698 698 ALKYLATION (SH-1) (POTENTIAL).
FT MOD_RES 708 708 ALKYLATION (SH-2) (POTENTIAL).
FT CONFLICT 15 15 A -> R (IN REF. 2).
FT CONFLICT 970 970 E -> Q (IN REF. 1 AND 4).
FT CONFLICT 1072 1072 M -> N (IN REF. 3).
FT CONFLICT 1247 1247 N -> H (IN REF. 1 AND 4).
FT CONFLICT 1251 1252 MC -> DGG (IN REF. 3).
FT CONFLICT 1261 1261 E -> G (IN REF. 1 AND 4).
FT CONFLICT 1297 1297 K -> Q (IN REF. 1 AND 4).
FT CONFLICT 1377 1378 KY -> NT (IN REF. 3).
FT CONFLICT 1504 1505 EN -> AH (IN REF. 1 AND 4).
FT CONFLICT 1847 1847 E -> D (IN REF. 1 AND 4).
FT CONFLICT 1914 1914 D -> H (IN REF. 2).
SQ SEQUENCE 1937 AA; 222762 MW; A3EE2D51792E9E8 CRC64;

Query Match 14.88; Score 176.5; DB 1; Length 1937;
Best Local Similarity 22.88; Pred. No. 0.045;
Matches 84; Conservative 53; Mismatches 97; Indels 135; Gaps 13;

QY 5 DSM-----VQSLDYTAQFEESYATLASEIEDIKLENSSIQEKARAGKNAE----DVQ 54
Db 1201 DSNALGEOIDNIDRVRQKLEKESEKLMETDLD-----SSNAAEISAKGULEMKCSLE 1256
QY 55 HOILATESNOEYBMLDLOTKSALKETEL-----KEIVSFL-----OKIT 97
Db 1257 DQSELTKEEEOORLINDLPAQARLOTAGEYSRQLEDERDALVSQLSRSKQASTQOIE 1316
QY 98 DLONOLKQOEED-----FRKQLEDEGRKAEKENTTAELTEEINKWRL 140
Db 1317 ELKHQLEETKAKNALAHALQSSRHQDCLREYEEQEKAEILOALSKANSVQAQMT 1376
QY 141 LY-----EELYNKTKRPOIQLD-----APEVEKQALNE----- 169
Db 1377 KYETDALQRTLEEAKKLAORLOEAEHEVEAVNACASLEKTKORLONEVEDLMJVE 1436
QY 170 -HGAAPQLKKIRDSYAKLIGHQNLKQ-----KIKHYVK----- 202
Db 1437 RSNAAACALDKKQRFNDKVLSEMKQYEETQALEASQKESRSLSTELFFVKVYESLD 1496
QY 203 ----LKDENSQKSEVSKLRQOLAK-----KKQ-----SETKLOE 233
Db 1497 QLETLRENNKNILOQELISDLTEQIABEGKQIHELEKTKKQYQEKCEIQAALFEAEASLEH 1556
QY 234 ELKKVVGIR 242
Db 1557 EEGKIIRIQ 1565

Search completed: July 17, 2003, 16:09:31
Job time : 15 secs

